IN THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

1-28. (Cancelled).

29. (Currently Amended) A process for the preparation and improvement of a pantothenic acid-producing microorganism comprising amplifying the endogenous panE gene in said microorganism and then incubating said microorganism under conditions suitable for the production of the panE gene product, ketopantoate reductase, wherein the ~~micoorganism~~ microorganism is selected from the group consisting of *Escherichia* and *Saccharomyces*.

30. (Currently Amended) The process of claim 29, wherein said panE gene is overexpressed in said ~~microogranism~~ microorganism.

31. (Cancelled).

32. (Previously Presented) The process of claim 29, wherein the ilvC gene is additionally amplified.

33. (Previously Presented) Te process of claim 30, wherein overexpression is achieved by insertion of a gene encoding a protein having ketopantoate reductase activity into a plasmid vector and then transforming said microorganism with said plasmid vector.

34. (Previously Presented) Te process of claim 33, wherein a promoter is incorporated upstream of said gene encoding a protein having ketopantoate activity.

35. (Cancelled).

36. (Previously Presented) The process of claim 30, wherein overexpression is achieved by mutating a promoter or other regulatory element controlling coding sequence of a structural gene that prompts pantothenic acid production, the promoter or other regulatory element being located upstream of the structural gene.

37. (Currently Amended) The process of claim 29, wherein the gene that codes for ketopantoate reductase is amplified in a microorganism that has one or more metabolite resistance mutations wherein the ~~micoorganism~~ microorganism is selected from the group consisting of *Escherichia* and *Saccharomyces*.

38. (Currently Amended) The process of claim 29, wherein the gene which codes for ketopantoate reductase is amplified in a microorganism, which has one or more antimetabolite resistance mutations wherein the ~~microogranism~~ microorganism is selected from the group consisting of *Escherichia* and *Saccharomyces*.

39. (Previously Presented) The process of either claim 37 or claim 38, wherein said microorganism is resistant to one or more compounds selected from the group consisting of: the metabolite L-valine; the metabolite alpha-ketoisovaleric acid; the antimetabolite salicyclic acid; the antimetabolite alpha-ketobutyric acid; beta-hydroxyaspartic acid; and the antimetabolite O-methylthreonine.

40. (Previously Presented) The process of claim 29, wherein said microorganism over-expresses at least one protein selected from the group consisting of: the protein having ketopantoate reductase activity encoded by the panE gene of *Escherichia coli*; the protein encoded by the ilvC gene of *Corynebacterium glutamicum*; and the protein having ketopantoate reductase activity encoded by the YHR063c reading frame of *Saccharomyces cerevisiae*.

41. (Previously Presented) The process of claim 29, wherein, additionally, at least one gene of the metabolic path of pantothenic acid formation is amplified.

42. (Previously Presented) The process of claim 41, wherein said gene of the metabolic path of pantothenic formation is selected from the group consisting of: ketopantoate hydroxymethyltransferase (EC 4.1.2.12); aspartate 1-decarboxylase (EC 4.1.11); isomero reductase; and pantothenate synthetase (EC 6.3.2.1).

43. (Currently Amended) The process of claim 41, wherein said ~~microogranism~~ microorganism is transformed with a plasmid vector comprising at least one gene of the

metabolic path of pantothenic acid formation selected from the group consisting of: ketopantoate hydroxymethyltransferase; aspartate 1-decarboxylase, isomero reductase, and pantothenate synthase.

44. (Previously Presented) The process of claim 29, wherein the activity of at least one gene in a metabolic pathway which reduces the formation of pantothenic acid is eliminated in said microorganism.

45. (Previously Presented) The process of claim 44, wherein the activity of the avtA gene is eliminated.

46. (Previously Presented) The process of claim 44, wherein the activity of the ilvE gene is eliminated.

47. (Previously Presented) The process of claim 29, wherein the ilvC gene of *C. glutamicum* is overexpressed or amplified in said microorganism.

48.-49. (Cancelled).

50. (Previously Presented) The process of claim 29, wherein said microorganism is a bacterium of the species *Escherichia coli.*

51.-53. (Cancelled).

54. (Previously Presented) The process of claim 29, wherein said microorganism is a yeast of the species *Saccharomyces cerevisiae.*

55. (Previously Presented) The process of claim 44, wherein said microorganism is *Escherichia coli* and the activity of either the avtA or ilvE gene is eliminated in said microorganism.

56. (Previously Presented) The plasmid vector pFE80 characterized by the restriction map shown in Figure 6 and deposited as *E. coli* K12 strain MG 1655/pFE80 under deposit number DSM 12414.

57. (Previously Presented) The plasmid vector pFE65, characterized by the restriction map shown in Figure 5 and deposited as *E. coli* K12 strain MG 1655/pFE65 under deposit number DSM 12382.

58. (Previously Presented) The plasmid vector pFE32, characterized by the restriction map shown in Figure 4 and deposited as *E. coli* K12 strain MG 1655/pFE32 under the deposit number DSM 12413.

59. (Previously Presented) The process of claim 29, wherein K12 strain FE6 is used, said strain being deposited under deposit number DSM 12379.

60. (Previously Presented) The process of claim 29, wherein *E. coli* K12 strain FE7 is used, said strain being deposited under deposit number DSM 12380.

61. (Previously Presented) The microorganism produced by the process of claim 29 wherein the microorganism is selected from the group consisting of *Eschericia and Saccharomcyes*.